If any matters remain before the present application is examined on the merits, the Examiner is invited to telephone the undersigned at the telephone number listed below.

Respectfully submitted,

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Marked-up Version of Amended Specification Pursuant to 37 C.F.R. §§ 1.121(b)-(c)

Replace the paragraph on page 3, lines 26-31, with the following:

FIG. 1 is a sequence comparison of an EDA1-II (EDA) (SEQ ID NO 2) and Tabby (Ta) (SEQ ID NO 2) proteins. Amino acid identities are indicated by an asterisk (*). The transmembrane domain is boxed. A vertical line designates the start of the protein sequence unique to isoform II. The Gly-X-Y domain is indicated by boldface type, with the 2-amino acid interruption indicated by shadowed lettering. A blackened circle is shown above two potential N-linked glycosylation sites, and three C-terminal cysteines are indicated by underlining and boldface type.

Replace the paragraph on page 4, lines 7-11, with the following:

FIG. 4 is a comparison of the sequences of the central β -sheet of EDA1-II (amino acids 291-309 of SEQ ID NO 2) compared with human tumor necrosis factor (Hu TNF, SEQ ID NO 123), lymphotoxin α (LT α , SEQ ID NO 124), lymphotoxin β (LT β , SEQ ID NO 125), FAS (SEQ ID NO 126), and CD40-L (ligand, SEQ ID NO 127), which are all members of the TNF family of proteins. One dot over a column indicates conservation across all sequences. Two dots over a column indicates the G(x)Y (glycine and tyrosine residues) identified in all the TNF related proteins.

Insert the following paragraphs on page 5, line 33:

SEQ ID NO 123 shows a portion of a human tumor necrosis factor protein.

SEQ ID NO 124 shows a portion of a human lymphotoxin α protein.

SEQ ID NO 125 shows a portion of a human lymphotoxin β protein.

SEQ ID NO 126 shows a portion of a human FAS protein.

SEQ ID NO 127 shows a portion of a human CD40-L protein.

Replace the paragraph on page 20, lines 9-14, with the following:

The EDA1-II cDNA (SEQ ID NO 1) encodes a 391 residue protein (SEQ ID NO 2), 256 amino acids of which are encoded by new exons. EDA1-II is 94% identical to Tabby (SEQ ID NO 4), and includes a collagen-like domain with 19 repeats of a Gly-X-Y motif, interrupted by

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two amino acids between repeats 11 and 12 (FIG. 1). The full-length EDA1-II transcript can include a longer 3' UTR, because no polyadenylation signal sequence was identified, and Northern analysis indicates the transcript is 5-6 kb in length. The *Tabby* transcript is also 5-6 kb in length and has a 3' UTR of approximately 3.5 kb.